

<!--StartFragment-->RESULT 1
 ADC00348
 ID ADC00348 standard; protein; 441 AA. APPENDIX B SEQ ID NO; 24
 XX
 AC ADC00348;
 XX
 DT 15-JUN-2007 (revised)
 DT 04-DEC-2003 (first entry)
 XX
 DE Enterohaemorrhagic E. coli O157:H7-specific protein SEQ ID NO: 393.
 XX
 KW enterohaemorrhagic; anti-bacterial; BOND_PC; hypothetical protein;
 KW hypothetical protein ECs1812 [Escherichia coli O157:H7];
 KW hypothetical protein ECs1812 [Escherichia coli O157:H7 str. Sakai];
 KW unknown protein encoded by cryptic prophage CP-933P;
 KW hypothetical protein [Escherichia coli O157:H7 str. Sakai].
 XX
 OS Escherichia coli; O157:H7.
 XX
 PN JP2002355074-A.
 XX
 PD 10-DEC-2002.
 XX
 PF 24-JAN-2002; 2002JP-00015959.
 XX
 PR 24-JAN-2001; 2001JP-00112010.
 XX
 PA (UYTS-) UNIV TSUKUBA.
 XX
 DR WPI; 2003-451640/43.
 DR PC:NCBI; gi13259568.
 XX
 PT Enterohemorrhagic Escherichia coli O157:H7-specific nucleic acid molecule
 PT and a polypeptide and its use, a polypeptide, a vector and a host cell.
 XX
 PS Claim 3; SEQ ID NO 393; 2067pp; Japanese.
 XX
 CC The invention relates to a novel enterohaemorrhagic Escherichia coli
 CC O157:H7-specific nucleic acid molecule. A polynucleotide of the invention
 CC has anti-bacterial activity. The polypeptide can be used in detection
 CC and/or treatment of O157:H7 infection. The nucleotide sequence of the
 CC genome of Enterohaemorrhagic E. coli O157:H7 was determined. The present
 CC sequence represents an E. coli O157:H7-specific polypeptide of the
 CC invention.
 CC
 CC Revised record issued on 15-JUN-2007 : Enhanced with precomputed
 CC information from BOND.
 XX
 SQ Sequence 441 AA;

Query Match 100.0%; Score 2341; DB 6; Length 441;
 Best Local Similarity 100.0%; Pred. No. 1.1e-197;
 Matches 441; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNIQPTIQSGITSQNNQHHQTEQIPSTQIPQSELPLGCQAGFVVNIPDDIQQHAPCGET 60
 |||||||
 Db 1 MNIQPTIQSGITSQNNQHHQTEQIPSTQIPQSELPLGCQAGFVVNIPDDIQQHAPCGET 60

Qy 61 TALLSLIKDKGLLGLDEYIAPHLEEGSIGKKTLDMFGLFNVNTQMALEIPSSVSGISGKY 120
 |||||||
 Db 61 TALLSLIKDKGLLGLDEYIAPHLEEGSIGKKTLDMFGLFNVNTQMALEIPSSVSGISGKY 120

Qy 121 GVQLNIVKPDIHPTSGNYFLQIFPLHDEIGFNFKDLGPLKNALSNSNISTAVSTIAST 180
 |||||||
 Db 121 GVQLNIVKPDIHPTSGNYFLQIFPLHDEIGFNFKDLGPLKNALSNSNISTAVSTIAST 180

Qy 181 GTSATTSTVTTEPKDPIPWFGLTAQVVRNHGVELPIVKTENGWKLVGETPLPDGPKANY 240

Db 181 GTSATTSTVTEPKDPIPWFGLTAQVVRNHGVELPIVKTENGWKLVGETPLTPDGPKANY 240
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Qy 241 TEEWVIRPGEADFKYGASPLQATLGLEFGAHFKWDLNDNPNTKYAVLTNAAANALGALGGF 300
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Db 241 TEEWVIRPGEADFKYGASPLQATLGLEFGAHFKWDLNDNPNTKYAVLTNAAANALGALGGF 300
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Db 301 AVSRFASTDPMSPHIGAMVGQAAGHAIQYNTPGLKPDТИLWWAGATLGAADLNKAEEFV 360
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Qy 361 ARFTDYPRIWWHAREGAIFPNKADIEHATGADIRAMEEGIPVGQRHPNPEDVVIDIESNG 420
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Db 361 ARFTDYPRIWWHAREGAIFPNKADIEHATGADIRAMEEGIPVGQRHPNPEDVVIDIESNG 420
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Qy 421 LPHHNPSNHVDIFDIIQETRV 441
|||
Db 421 LPHHNPSNHVDIFDIIQETRV 441
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